#### IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

STEPHEN M. ALLEN ET AL. CASE NO.: BB1210 US DIV

APPLICATION NO.: UNKNOWN GROUP ART UNIT: UNKNOWN

FILED: HEREWITH EXAMINER: UNKNOWN

FOR: NITROGEN TRANSPORT METABOLISM

#### PRELIMINARY AMENDMENT

Commissioner for Patents Washington, DC 20231

Sir:

Prior to examination, please amend the captioned application as follows and consider the following remarks.

#### IN THE SPECIFICATION:

## Please replace the following paragraphs:

### Paragraph beginning at page 1, line 3:

This application is a division of U.S. Application No. 09/384,625 filed August 27, 1999, which claims the benefit of U.S. Provisional Application No. 60/098,248, filed August 28, 1998.

## Paragraph beginning at page 8, line 4:

"Codon degeneracy" refers to divergence in the genetic code permitting variation of the nucleotide sequence without affecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention relates to any nucleic acid fragment comprising a nucleotide sequence that encodes all or a substantial portion of the amino acid sequences set forth herein. The skilled artisan is well aware of the "codon-bias" exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid fragment for improved expression in a host cell, it is desirable to design the nucleic acid fragment such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

#### IN THE CLAIMS:

#### Please cancel claims 1-21. Please add the following claims:

- 22. "added" An isolated polynucleotide comprising:
- (a) a nucleotide sequence encoding a polypeptide having ammonium transporter activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 80% sequence identity based on the Clustal alignment method, or

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(b) the complement of the nucleotide sequence, wherein the complement and the nucleotide sequence contain the same number of nucleotides and are 100% complementary.

- 23. "added" The polynucleotide of Claim 22 wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 90% sequence identity based on the Clustal alignment method.
- 24. "added" The polynucleotide of Claim 22 wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 95% sequence identity based on the Clustal alignment method.
- 25. "added" The polynucleotide of Claim 22 wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:4.
- 26. "added" The polynucleotide of claim 22 wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:3.
  - 27. "added" A vector comprising the polynucleotide of Claim 22.
- 28. "added" A recombinant DNA construct comprising the polynucleotide of Claim 22 operably linked to a regulatory sequence.
- 29. "added" A method for transforming a cell comprising transforming a cell with the polynucleotide of Claim 22.
  - 30. "added" A cell comprising the recombinant DNA construct of Claim 28.
- 31. "added" A method for producing a plant comprising transforming a plant cell with the polynucleotide of Claim 22 and regenerating a plant from the transformed plant cell.
  - 32. "added" A plant comprising the recombinant DNA construct of Claim 28.
  - 33. "added" A seed comprising the recombinant DNA construct of Claim 28.
- 34. "added" An isolated polynucleotide comprising a first nucleotide sequence, wherein the first nucleotide sequence contains at least 30 nucleotides, and wherein the first nucleotide sequence is comprised by another polynucleotide, wherein the other polynucleotide includes:
- (a) a second nucleotide sequence, wherein the second nucleotide sequence encodes a polypeptide having ammonium transporter activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 80% sequence identity based on the Clustal alignment method, or
- (b) the complement of the second nucleotide sequence, wherein the complement and the second nucleotide sequence contain the same number of nucleotides and are 100% complementary.
- 35. "added" A method for isolating a polypeptide encoded by the polynucleotide of Claim 22 comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide operably linked to a regulatory sequence.

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REMARKS

Claims 1-21 have been canceled and claims 22-35 added. The newly added claims are drawn to the invention of Group I (polynucleotide) and (b) (SEQ ID NO:3 or a sequence encoding SEQ ID NO:4) of the restriction requirement mailed December 12, 2000 in the parent application, U.S. Application No. 09/384,625. No new matter is added by the addition of claims 22-35.

Entry of the amendments and favorable consideration of the claims are respectfully requested.

Respectfully submitted,

PAUL D. GOLIAN

ATTORNEY FOR APPLICANTS

REGISTRATION NO. 42,591

TELEPHONE: (302) 992-3749 FACSIMILE: (302) 892-1026

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# **VERSION WITH MARKINGS TO SHOW CHANGES MADE**

In showing the changes, deleted material is shown as brackets, and inserted material is shown underlined.

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#### IN THE CLAIMS:

Claims 1-21 canceled.

Claims 22-35 added.